

FIGURE 1

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT
GTTGAAGGGTGTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTCTTACACAGTG
TCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATAAATCTACTTTTAGGAGGA
CTACTCTCTTCTGACAGTCTAGACTGGTCTTCTACACTAAGACACCCATGAAGGAGTATGTG
CTCCTATTATTCTGTGCTTTGTGCTCTGCCAAACCCCTCTTTAGCCCTTCACACATCGCACT
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATG
ATGATGATGATGAGGACAACCTCTCTTTTCCACAAGAGAGGCCAAGAAGCCATTTTTTCCA
TTTGATCTGTTTTCCAATGTGTCCATTTGGATGTGAGTGCTATTACGAGTTGTACATTGCTC
AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCATTTGATACCGAATGCTTGATCTTC
AAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAGGACTCACTTCACCTTTATGGT
CTGATCCTGAACAACAACAGCTAACGAAGATTCAACCAAGCCCTTCTAACCCACAAGAA
GTTGCGAAGGCTGTATCTGTCCCAACATCAACTAAGTGAAATACCACTTAATCTTCCCAAT
CATTAGCAGAATCAGAAATTCATGAAAAAAGTTTAAAGAAAATACAAAAGGACACATTTCAA
GGAATGAATGCTTTTACAGCTTTTGGAAATGAGTGCAACCCCTCTTGATAATAATGGGATAGA
GCCAGGGGCATTTGAAGGGGTGACGGTGTTCATATCAGAATTGCAGAAGCAAACTGACCT
CAGTTCTTAAAGGCTTACCACCACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA
ACAGTGGAACTTGAGGATTTTAAACGATACAAAGAACTACAAGGCTGGGCCCTAGAGCAACA
CAAAATCAGAGATATCGAAAATGGGAGTCTTGCTAACATACCAGTGTGAGAGAAAATACATT
TGGAAAACAATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA
ATCTTCTTCATTCTAATTCAATTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCC
AAAGATGAAGAAATCTTTATACAGTGAATAAGTTTATTCAACAACCCGGTGAAATCTGGG
AAATGCAACCTGCAACATTTCTGTGTGTTTTGAGCAGAATGAGTGTTCAGCTTGGGAACCTT
GGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACATT
TGGAACTCTGAACCTATTAATAATGGTAGTATTATATATACAAAGCAATATCTATTCTCA
AGTGGTAAGTCCACTGACTTATTTATGACAAGAAATTTCAACGGAATTTGCCAAACTATT
GATACATAAGGGGTGAGAGAAAACAAGCATCTATTGCAGTTTCTTTTTTGCGTACAAATGAT
CTTACATAAAATCTCATGCTTGACCATTCCTTTCTTCATAACAAAAAGTAAGATATTCGGTA
TTTAAACACTTTGTATCAAGCACATTTTAAAAAGAACTGTACTGTAATGGAATGCTTGACT
TAGCAAAATTTGTGCTCTTTCATTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGT
GAAGAGTGCATTACACTATTTCTTATTCTTTAGTAACCTGGGTAGTACTGTAATTTTTTAAT
CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGT
CTTTATGTTTAAACTAAATTTCTTAAATAAAGCCCTCAGTAAATGTTTCATTACCAACTTGA
TAAATGCTACTCATAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTAAATTATT
ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAACCTCGCATTT
AATGATCCGCTATTATAAGCTTTAATAGCATGAAAAATGTTAGGCTATATAACATTGCCAC
TTCACTCTAAGGAATATTTTTGAGATATCCCTTTGGAAGACCTTGCTTGGAGAGCCCTGGA
CACTAACAAATCTACACCAAAATGTCTCTTCAAATCGTATGAGCTGGATAACTCTGAGAAA
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAACAGACAGAAACCGAAAGCTCTA
TATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCAACATATGTAAAAATCAGAAA
ACAGGGAAATTTTCATTAATAAAATATTGGTTTGAAT

03943730.033001

FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDEDNSLFPTREPR
SHFFPFDLFPMPGFCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNKKLTKIHKPAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ
KDTFGKGMNALHVLEMSANPLDNNGIEPGAPEGVTVPFHIRIAEAKLTSVPKGLPPTLLEHLHD
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLNKKLKKIPSGLPPEL
KYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCLSRMSV
QLGNFGM

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLGLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRGAAGCTFGGKVYALDE
TWHPDLGQPPFGVMRCVLCACEAPQWGRTRGPGRVSCNLIKPECPTPACGQPRQLPGHCCQT
CPQERSSSERQPSGLSFEYPRDPEHRSYSYDRGEPGAERARGDGHGTFVALLTGPRSQAVAR
ARVSLRLSSSLRFSISYRRLLDRPTRIRFSDSNGSVLFEHPAAPTQDGLVCGVWRAPRLSLRL
LRAEQLHVALVTLTHPSGEVWGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTSLDTE
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGQLLRELQANVSAQEPGFAEVLNLTVMQEMD
WVLGELQMALEWAGRPGLRISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN
GSLIYQVQVVGTSSEVAMTLETKPQRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML
LQNELFLNVGTKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVVKSAAGHAWLS
LDTHCHLHYEVLLAGLGSEQGTVTAHLGLPGPTPGPRRLKGFYGSEAQGVVKDLEPELLR
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGGRLLEAAGAEGVRALGAPDTASAAPPVV
PGLPALAPAKPGGPGPRPDNTCFEFGQQRPHGARWAPNYDPLCLSLCTQRRRTVICDPVVCP
PPSCPHVPQADQCCPVCPEKQDVDRDLPLGLPRSRDPGEGCYFDGDRSWRAAGTRWHVPPVPPF
GLIKCAVCTCKGGTGEVHCCKGVQCPRLACAQPVVRNPTDCKKQCPVGS GAHPQLGDDPMQADG
PRGCRFAGQWFPESQSWHPVSVPPFGEMSCITCRGAGVPHCERDDCSLPLSCSGSKESRCCS
RCTAHRPPETRTDPELEKEAEGS

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

Figure 1

[illegible]

FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQQLPALALLLLLLLGGAGPRGSSSLANVPVPAAPLSAPGPCAAQPCRNGGVCTSR
PEPDQHPAPAGPEGYSCTCPAGISGANCLVADPCASNPCHHGNCSSSSSSSSSDGYLCICN
EGYEGPNCEQALPSLPATGWTESMAPRQLQVPVATQEPDKILPRSQATVTLPTWQPKTGQKV
VEMKWDQVEVIPDIACGNASSNSAGGRLVSPFVQNTSVKIRODATASLILLWKVTATGFQ
QCSLIDGRSVTPLQASGGLVLLLEMLALGNNHFIGFVNDSVTKSIVALRLTLVVKVSTCVPG
ESHANDLECSGKGKCTTKPSEATFSCTEEYVGTFCCEEYDACQRKPCQNNASCIDANEKQD
GSNFTCVCLPGYTGLCQSKIDYCILDPNRGATCISLSGFTQCCEGYFGSACEEKVDPC
ASSPCQNNGTCTYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSYKCLCDPG
YHGLYCEEEYNECLSAFCLNAATCRDLVNGYECVCLAEYKGTHCELYKDPKANVSCNLGATC
DSDGLNGTICICAPGFTGEECDIDINECDSPNCHHGSSCLDQPNGYNCHCPHGWVGANCEIHL
QWKSGHMAESLTNMPRHSYIIIGALCVAFILMLIILVIGICRISRIEYQSSSRPAYEEFYN
CRSIDSEFSNAIASIRHARFGKSRPAMYDVSPAIYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

FIGURE 7

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTC
AGGAAAAGGAAAATGCACCACGAAGCCGTGAGAGGCAACTTTTTCCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTCACCTGTGTTTGCCTTCC
TGTTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

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CTCTGGAAGGTCACGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGACCCCCCTTTCAGGCTTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAAATAATCACTTTATTGGTTTGTGTAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACTCTGGTGGTGAAGGTCAGCACTGTGTGCCGGGGGAGAGTCA CGCAAATGACTTGGAGTGTTCAGGAAAAGGAAAAATGCACCACGAAGCCGTGAGAGGCAACTTTTCTGTACTCTGTGAGGAGCAGTACGTGGGTACTTTCTGTGAAGAAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAACGCGAGCTGTATTGATGCAAAATGAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC TGGTTATATCGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACTGAGTAGATGGGGAG

FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG
GCCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCACACC**ATG**CCGGGCACCTAC
GCTCCCTCGACCACACTCAGTAGTCCACGACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT
GATGCGGGACTTCCCGCTCGTGAGCGGCCACAACGACCTGCCCCCTGGTCTTAAGGCAGGTTT
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTAGCTACGGCCAGACCAGCCTGGAC
AGGCTTAGAGATGGCCTCGTGGGCGCCAGTTCTGTGCAGCCTATGTGCCATGCCAGACCA
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCGATGTGTGCCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCTCATCGGTGTAGAGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
CTACATGCTGGGAGTGCCTACCTGACGCTCACCACACCTGCAACACACCCTGGGCAGAGA
GCTCCGCTAAGGGCGTCCACTCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG
AAGGTGGTGGCAGAAATGAACCGCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCC
GGGTGTGTGCAACAGTGTCTCGGAATGTTCTGTATGACATCTTCAGAGCTTCTGAAGAAGAAC
GGTGGCGTCGTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGC AACCCATCAGCCAATGT
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCTATTGGATCCAAGTTCATCGGGA
TTGGTGGAGATTATGATGGGGCCGCAAAATTCCTCAGGGGCTGGAAGACGTGTCCACATAC
CCGGTCTCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTC
TCGTGGAAACCTGCTGCGGTCTTCAGACAAGTGGAAGAGGTACAGGAAGAAAACAAATGGC
AAAGCCCCTTGGAGGACAAGTTCCTGGATGAGCAGCTGAGCAGTTCTGCCACTCCGACCTC
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACCTACTGAGATCCCATACA
CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCTCCCCCACATGGCCCCAG
TCCTTGCAGTTGTGGCCACCTTCCAGTCCTTATTCTGTGGCTC**TGA**TGACCCAGTTAGTCC
TGCCAGATGTCACTGTAGCAAGCCACAGACCCCCACAAAGTTCCCTGTGTGCAGGCACA
AATATTTCTGAAATAAATGTTTTGGACATAG

0943736.03001

FIGURE 10

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595
<subunit 1 of 1, 433 aa, 1 stop
<MW: 47787, pI: 6.11, NX(S/T): 5
MPGTYAPSTTLSSPSTQGIQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
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TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL
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N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

FIGURE 11

AAAACCTATAAATATTCCGGATTATTCATACCGTCCCACCATCGGGCGCGGATCCGCGGCCG
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA
CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATCGGGGACTTCCCGCTCGTGGACGGCCAC
AACGACCTGCCCTTGGTCTTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTTAACCTGCG
CAATTTCAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCAGT
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGATGCCCTGCGCCTCACCTGGAG
CAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC
TAAAGCTCTGAACGCACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCCTACCTGACGCTC
ACCCACACCTGCAACACACCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGGCA
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCAGGCGGGGCCCTGGAAGTGTACAG
GCACCTGTGATCTTCTCCCACTCGGCTGCCCGGGGTGTGTGCAACAGTGCTCGGAATGTTCC
TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTGTCCATGG
GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC
AAGGCTGTCTTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT
CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCTGATAGAGGAGTTGCTGAGTCGTG
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTTCGTGGAAACCTGCTGCGGGTCTTCAGACAA
GTGGAAGAGGTACAGGAAGAAAACAAATGGCAAAGCCCTTGGAGGACAAGTTCCTGGATGA
GCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCAGCTCTGCGTCAGAGACAGAGTCTGACTT
CAGGCCAGGAACCTCACTGAGATTCCCATACACTGGACAGCCAAGTTACCAGCCAAGTGGTCA
GTCTCAGAGTCTCCCCCACCCTGACAAAACCTCACACATGCCACCCTGCCAGCACCTGA
ACTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACAC

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><subunit 1 of 1, 446 aa, 0 stop

><NX (S/T) : 5

MPGTYAPSTTLSSPSTQGLQEQARALMRDFFLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDLSLSILRTFYMLGVRVYLTLTHTCNTFPWAESSAKGVHSFYNNISGL
TDFGEKVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGV IQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYFVLIEELLSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSS
CHSDLSRLRQQLSLTSGQELTEIPIHWTAKLPAKWSVSESSPHDKTHTTCCPAPPELLGGP
SVLFPPPKPKDT

FIGURE 13

CGCCAGCGACGTGCGGGCGGCTGGCCCGCGCCCTCCCGCGCCCGGCTGCGTCCCGCGCC
 CTGCGCCACCGCCGCCGAGCGCAGCCCGCGCGCGCCCCCGGACGCGCGGCCCC**ATG**CCC
 GCGGGCGCGCGGGGCCCGCGCCCAATCCGCGGGCGGCGCGCGCGT**TG**CGCCCTGCT
 GCTGCTGCTCTGCGTCTCTCGGGCGCGCGAGCCGGATCAGGAGCCACACAGCTGTGATCA
 GTCCCCAGGATCCACGCTTCTCATCGGCTCTCCCTGCTGGCCACCTGCTCAGTGACAGGA
 GACCCACCAGGAGCCACCGCGAGGGCTCTACTGGACCTCAACGGGCGCGCCCTGCCCCC
 TGAAGCTCTCCGTGTACTCAACGCTCCACCTTGGCTCTGGCCCTGGCCAACCTCAATGGT
 CCAGGCAGCGTGGGGGACAACCTCGTGTGCCACGCCGTGACGGCAGCATCTGGCTGGC
 TCCTGCCCTCTATGTTGGCTGCCCCAGAGAAACCGTCAACATCAGTGTCTGGTCCAAGAA
 CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCACGGGAGACCTTCTCCACACCA
 ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGGCCAGGACAACATGTGAGGAGTACCAC
 ACAGTGGGGCCCCACTCTGCGCATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGAT
 CTGGGTGGAGGCCAACCGCTGGGCTCTGCCGCTCCGATGTACTACGCTGGATATCC
 TGGATGTGGTGACCACGGACCCCCCGCCGACGTGCACGTGAGCCGCGTGGGGGCTGGAG
 GACCAGCTGAGCGTGCCTGGGTGTGCCACCCGCCCTCAAGGATTTCTCTTTCAAGCCAA
 ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGAGCA
 ACCAGACCTCTGCGCCTGGCCGGCTGAAACCCGGCACCGTGTACTTCTGTCAAGTGGC
 TGCAACCCCTTTGGCATCTATGGCTCCAAGAAAGCCGGGATCTGGAGTGAGTGGAGCCACC
 CACAGCCGCTCCACTCCCGCAGTGAGCGCCCGGGCCCGGGCGGCGGCGTGCGAACCGC
 GGGGCGGAGAGCCGAGCTCGGGCCCGTGCGGCGGAGCTCAAGCAGTTCTGGGCTGGCTC
 AAGAAGCACGCGTACTGCTCCAACCTCAGCTTCCGCTCTACGACCAGTGGCGAGCTGGAT
 GCAGAAGTCGCACAAGACCCGAACCCAGGACGAGGGGATCTGCCCTCGGGCAGACGGGGCA
 CGGCGAGAGGTCTGCCAG**TAA**AGCTGTAGGGGCTCAGGCCACCTCCCTGCCACGTGGAGA
 CGCAGAGGCCGAACCCAACTGGGGCCACCTCTGTACCCTCACTTCAGGGCACCTGAGCCAC
 CCTCAGCAGGAGCTGGGGTGGCCCTGAGCTCCAACGGCCATAACAGCTCTGACTCCACGT
 GAGGCCACCTTTGGGTGCACCCAGTGGGTGTGTGTGTGTGTGAGGGTTGGTTGAGTTGC
 CTAGAACCCCTGCCAGGGCTGGGGGTGAGAAGGGAGTCATTACTCCCATTAACCTAGGGCC
 CCTCCAAAAGAGTCTTTTAAATAAATGAGCTATTTAGGTGCTGTGATTGTGAAAAA
 AA

FIGURE 14

><ss.DNA38113
><subunit 1 of 1, 422 aa, 1 stop
><MW: 46302, pI: 9.42, NX(S/T): 6
MPAGRGRGPAQAQARRPPPLLLPLLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATCSV
HGDPPGATAEGLYWTNLRRLPPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL
AGSCLYVGLPPEKFPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEE
YHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVS RVGG
LEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVDDVSNQTSCLAGLKPGTVYFVQ
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGACEPRGEPSSGPVRELKQFLG
WLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRRGTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

100582 "027E+66
004137203 003001

[illegible][illegible]

FIGURE 16

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

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YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

00000000

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCGCGGACGGAGCGAACCAAGGACTG
GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAAGCGCGGGGGCTGGAGCACCACCAA
CTGGAGGGTCCGGAGTAGCGAGCGCCCGGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT
GCGAGAGGACCCCGGCGTCCGGGCTCCCGGTGCCAGCGCTATGAGGGCCTCTCTGTCCTGC
TGCTCCTGGGCTTGGCGGCCGGCTCGCCCCACTTGGACGACAACAAGATCCCCAGCCTCTGC
CCGGGGCACCCCGGCCCTTCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGCCG
CGATGGCCCGCAGCGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGCGAGGGCGGGA
GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGG
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AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTCTGCCCCAGACCA
GAGGAGTGTGCTGTGCTGGCAAGTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT
GGGGTGCTCTCTTCTGGTCTCTGCTTCTCTGGATCTCCCCACCCCTCTGCTCTTGGG
GCCGGCCCTTTCTCAGAGATCACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FOR THE RECORD

><subunit 1 of 1, 243 aa, 1 stop

MRPLLVLVLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHSQGLPGRDGRDGRDGA
GEKGEGRPGLPGRDGPGRGEAGPAGTPGAGECSVPPRSAPSAKRSESRVPPSPDAPLP
FDRVLVNEQGHYDAVTGKFTCQVPGVYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPSALSGGAMVRLEPEDOVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

FIGURE 19

CTCTTTTGTCCACCAGCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAG
CCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCTG
CAAGTGGGCTGGAACATGCAGCTGCTGCCCGGGCTTGGCGTCTTTGTTGAAGTGGTCAG
CCTATGTTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGCGGCAC
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCCGAGGCCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGTGCCTGGTGTTCTGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGCTCTGTGAGGTCCCC
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATTGGACGTCTCAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC
ACGGCCGGTTCGGGAGGAGGAGTGTCTGTGCTCTGTGACATCGGCTACGGGGGAGCCAG
TGTGCCACCAAGGTGCATTTTCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTGAGAGGAAAGGCG
GGGTGTGGCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGC
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTCTGGATCGGGCT
CACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACAGGCCCTTACCA
GTTTTTGCTTTGGGCAGCCTGACAACCACGGGCTGGTGTGGCTGAGTGTGCCATGGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTTCAGTGCCTTCAACTGGAACGACAGCGCTGCAAAAC
CCGAAACCGTTACATCTGCCAGTTTGCCAGGAGCACATCTCCCGTGGGGCCAGGGTCTT
GAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGA
CCTTGACAATGCCAGAAGTTGGGCAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG
AGTGTTAGAAGAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAAGGCTGCTCTCTTCCACCTGGCCAGAC
CCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCACGGGTATTAAATTATGAATCAG
CTGAAAAAAAAAAAAA

FIGURE 21

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCCGCGGGGTCCCCGAGCGTCCCGCGCCCT
CGCCCCGCC**ATG**CTCCTGCTGCTGGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTCGCA
GGAAGAGGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGATCAGGGTCCCGAGGCAAG
TCAGACTGTTGTCAGAGGCTGAAAACCAAACCTTTGATGACAGAATTCTCAGTGAAGTCTACC
ATCATTTCCCGTTATGCCTTCACTACGGTTTCTGTCAGAATGCTGAACAGAGCTTCTGAAGA
CCAGGACATTTAGTTCAGATGCAGATTCAGCTGCAGCTTTCATCACCACCTTCACTATGC
TTATTGGAGCAAGGTGTATCAGGGCCGAAATTACAGAGAGAGAAAAAGAGTGGTGATAGG
GTAAAGCAGAAAAAGAAATAAAACCCACAGAAGAAAATGGAGAGAGGGGACTGAAAATATTACAG
AGCTTCTGCAGTGATTCCACAGCAAGGACAAAGCCGCCCTTTTCCTGAGTTATGAGGAGCTTC
TGCAGAGGCGCCTGGGCAAGTACGAGCACAGCATCAGCGTGCGGCCCCAGCAGCTGTCCGGG
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC
GCTTCACAACAGCAGGCGAGAGGGGCGAGTGGGCGCGGGGAAGATGATTCTGGGCCTCCCCAT
CTACTGTCAATAACCAAAATGAAACATTTGCCAACATAATTTTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCCAGAAATGGAATTTGGGAGACTTTATCATTAGATATGACGTCATATAG
AGAACAGAGCATTTGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTTGCTCCTA
AAGACCTTCCTCCTTTACCCAAGAAATGTGGTATTCTGTGCTTGACAGCAGTGCTTCTATGGTG
GGAACCAAACTCCGGCAGACCAAGGATGCCCCTCTTCACAATTCTCCATGACCTCCGACCCCA
GGACCGTTTCAGTATCATTTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCACCTTGATAT
CAGTCACTCCAGACAGCATCAGGGATGGGAAGGTGACATTCACCATATGTACCCCACTGGA
GGCACAGACATCAACGGGGCCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCCA
CAGTGGCATTTGGAGACCGGAGCGTGTCCCTCATCGTCTTCTGACGGTGGGAAGCCACGG
TCGGGGAGACGCACCCCTCAAGATCCTCAACAACACCCGAGAGGGCCCGGAGGCCCAAGTC
TGCATCTTCACCATTTGGCATCGGCAACGACGTGGACTTCAGGCTGTGAGAGAACTGTCTGCT
GGAGAACTGTGGCCTCACACGGCGCGTGCACGAGGAGGAGGACGACGCTCGCAGCTCATCG
GGTTCTACGATGAAATCAGGACCCCGCTCCTCTCTGACATCCGCATCGATTATCCCCCAGC
TCAGTGTGTGACGGCCACCAAGACCTGTTCGCCCACTACTTCAACGGCTCGGAGATCATCAT
TGCGGGGAAGCTGGTGGACAGGAAGCTGGATCACCTGCACGTGGAGGTCACCGCCAGCAACA
GTAAGAAATTCATCATCTGAAGACAGATGTGCCTGTGCGGCCTCAGAAGGAGGGGAAAGAT
GTCACAGGAAGCCCGGCTGGAGGCGATGGAGAGGGGGACCAACCAATCTGAGCGTCT
CTGGAGCTACCTCACCAAAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTGACGATGAACCGG
AGAAGGAGCGGCTGCGGCAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCCTCACTCCC
TTCACTTCATGAAGCTGAGGGGGCCGGTCCACGATGGATGGCCTGGAGGAGGGCCACGG
CATGTGCGCTGCCATGGGACCCGAACCGGTGGTGCAGAGCGTGGGAGGAGCTGGCAGCGAGC
CAGGACCTTTGCTCAAGAAGCCAAACTCCGTCAAAAAAACAACCAACCAAAAAAAGA
CATGGGAGAGATGGTGTCTTCTCCTCCACACCTGGGGATACGAT**TGA**GAAGATGGCCACCT
GCAAGCCAGGAAGACGGCCTCACACAGACCATGTCTGCTGGCACCTTGATCTTGGACCTC
CCAGCCTCCAGAACTGTGAGAAATAATGTGTCTTTGTTAAGCTAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

09:47:30.03001

FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLQLRKTPLMTEFSVKSTIIS
RYAFTTVSCRMNLRASEQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE
KRNKTTENGEKGTIEFRASAVIPSKDKAAFFLSYEELLQRRLLGKYEHSISVRPQQLSGRLS
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPSTVINQNETFANIIIFKPTVVQQAR
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVFVLDSSASMGVTK
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVKDHLISVTPDSIRDGKVIYIHHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKLINNTREAAARGQVCIF
TIGIGNDVDFRLLKLSLENCGLTRRVHEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEIIAGKLVDRKLDHLHVEVTASNKKFIILKTDVPVRPQKAGKDV TG
SPRPGDGEGDTNHIERLWSYLTTELSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLKKPNVSVKKKQNKTKKRHGR
DGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

1-694 aa, 1 stop

FIGURE 23

CGGACGCGTGGGGTGCCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC
GGCAGCGGGCGGCGCGCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGG
CACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTAGCTACTGAA
TCCCAACAGGCAGACCATTATTTTCAGGGACTTCAGGCCCTTTGAAGGACAGCAGGTTTCAGT
TGCTGAATTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGT
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAA
GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG
AGCACCTTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGACATTCAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA
GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATG
ATGAAATGCCTCAACACGCCGTAAGTGTCTGGGCCCAACCTGTTTCATCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCACAACCTATCCCTCTCCACAACAACCACCACCACCA
CCACCACCACCACCACCACCATTACCATCATCACAGATTCCTGAGCAGGTGAAGAAGGC
TCGATCAGGCGAGTGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCAT
GCTGTGCTTGCTCATATTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA
GGACAGAACTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCCTTTTGTTCAT
GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

0943750.087001

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518

<subunit 1 of 1, 440 aa, 1 stop

<MW: 48240, pI: 4.93, NX(S/T): 7

MASVVLPSGSQCAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSLTNVISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG
KSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTRYLEVQYKPQVHIQMT
YPLQGLTREGDALELTCEAIGKQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYR
CEASNIVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTILTIIITDSRAGEEGSIRAVDH
AVIGGVVAVVVFAMLCLLIILGRYFARHKGTFTHEAKGADDAADADTAIINAEGGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

0047267.083001

FIGURE 25

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGA
 CCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCGCCCGGCTCCCTGCGCCGCCCGCCCTC
 CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT
 GGGGCCCTGGGGTGCAGGGCTGCCATCCGGCTGCCAGTGACAGCCAGCCACAGACAGTCTTCT
 GCACTCCCCGCCAGGGGACCAGGTTGCCCGAGACGTGCCACCCGACACGTTGGGGCTGTAC
 GTCTTTGAGAACGGCATCACCATGTCTCGACGCAAGCAGCTTTGCCGGCTGCCGGCCCTGCA
 GCTCTTGAGCTCTGCA CAGAACCAGATCGCCAGCCTGCCCGCTGCCCGCTGCTGCTGTCTGG
 ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAG
 GCGCTCGGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCG
 CAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG
 GCCTCCGGGGCTGACGCGCTGCGGCTGGCCGGCAACACCCGCATTGCCAGCTGCGGCC
 GAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC
 CCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCTGCGGCTGCTGGCAGTGCCTCGCAAC
 CCTTTCAACTGCGTGTGCCCTGAGCTGGTTTGGCCCTGGGGTGGCGGAGAGCCACGTCA
 CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCT
 GGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCACCACCAAGCCACAGTGCCACCA
 CGAGGCCGCTGGTGGCGGAGCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGC
 CCCACAGCGCCGGCCACTGAGGCCCCAGCCCGCCTTCACTGCCCCACCGACTGTAGGGCC
 TGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGG
 GGACACGGCACCCACTGGCGTGTCTGTGCCCCGAAGGCTTACGGGCCCTGTACTGTGAGAGC
 CAGATGGGGCAGGGGACACGCGCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCT
 GACCCTGGGCATCGAGCCGCTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCC
 AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
 AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCAACCAGCTGCG
 GCCCAACGCCACTTACTCCGTCTGTGTATGCTTTGGGGCCCGGGCGGGTGCAGGGGCG
 AGGAGGCTGCGGGGAGGCCCATACACCCAGCCGCTCCACTCCAACCAAGCCAGTCACC
 CAGGCCCGCAGGGCAACTGCGCGCTCCTCATGCGCCCGCCCTGCGCGGCTGCTCCTGGC
 CGCGCTGGCTGCGGTGGGGGAGCCTACTGTGTGCGGGCGGGGGCGGGCATGGCAGCAGCG
 CTCAAGACAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTTGAAGTGGAGGGAGTGAAGGTC
 CCCTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGCTGTGA
 GTGTGAGGTGCCACTCATGGCTTCCAGGGCCTGGCCTCCAGTACCCCTCCACGCAAGC
 CCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGC
 CAGCCCCCTCTGCTGCCACACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGACAG
 CAGGCTGTGTGACCAAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG
 ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCAGAACCGAGTGCCATGAGGACAGTGT
 CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGCCCTGCCATGTGCTGGTAAC
 GCATCCCTGGGCCCTGCTGGGCTCTCCACTCCAGCGGACCCCTGGGGCCAGTGAAGGAAG
 CTCCCGGAAAGAGCAGAGGGAGAGCGGTAGGGCGCTGTGTGACTCTAGTCTTGGCCCCAGG
 AAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAACATGTTTGGCTTTTAA
 AATATATATATATTATAAGAGATCCTTTCCCATTTATCTGGGAAGATGTTTTCAAACTC
 AGAGACAAGGACTTTGGTTTTTGAAGACAAACGATGATATGAAGGCCTTTTGAAGAAAAA
 ATAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVP LLLP LLLLL LALGPGVQGCPSGCQCSQPQT V FCTARQGT T VPRDVPDP T VGLYVFEN
GITMLDASSFAGLPGLQLLDLSQNIASLR LPR LLLDL SHNSLLALEPGILD TANVEALRL
AGLGLQQLDEGLF S RLRNLHLDLVDNQLERVFPVIRGLRGLTRLR LAGNTRIAQLRPEDLA
GLAALQELDVSNLSLQALPGDLSGLFPRLRL LAAARNPFNCVCPLSWFGPWPVRESHVTLASP
EETRCHFP PKNAGRL LLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPT WLSPTAP
ATEAPSP P P STAPPTVGPVPQPDCCPPSTCLNGGTCHLGRHHLACLCEGFTGLYCESQMGQ
GTRPSP T PVT PRPPRS LTLGIEPVSP TSLRVGLQRYLQGS SVQLRSLRLTYRNLSGPDKRLV
TLRLPASLA EYTVTQLRP NATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE
GNLP LLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGVGP GAGP LELEGVKVPLEP
GPKATEGG EALPSGSECEVPLMGFP GPGLQSPLHAKPYI

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

0943730103403

FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCGTACCCCTACCCGCCCGCCACC
TCCTTGCTACCCCACTCTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTCATGCCAGCCTC
ATCTCCTTTCTTGCTAGCCCCCAAAGGGCTCCAGGCAACATGGGGGGCCAGTCAGAGAGC
CGGCACCTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGCCGTGGCTTGTC
ATGGCTCTGCTGACCCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
GGGGACAGGAGGCCCTCCAGAATGGGGAAGGGTATCCCTGGCAGAGTCTCCCGAGCAGA
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC
ACCCAAAAACAGAAGAAGCAGCACTCTGTCTGCACCTGGTTCCTAATAACGCCACCTCCAA
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCTAC
AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC
CTGTTTCAAGACGTGACTTTCACCATGGGTGAGTGGTGTCTCGAGAAGGCCAAGGAAGGCA
GGAGACTCTATTCGATGTATAAGAAGTATGCCCTCCACCCGGACCGGGCTTACAACAGCT
GCTATAGCGCAGGTGTCTTCCATTACACCAAGGGGATATTCTGAGTGTACATAATTCCCCGG
GCAAGGGCGAAACTTAACCTCTCTCCACATGGAACCTTCTGGGGTTTGTGAAACTGTGATT
GTGTTATAAAAAGTGGCTCCAGCTTGGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA
GAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCTGGGTTTGGCTC
CCCGTTCTCACTTTTCCCTTTTCATTCCACCCCTAGACTTTGATTTTACGGATATCTTG
CTTCTGTTCCCCATGGAGCTCCG

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

MPASSPFLAPKGPPEGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTTELQSLRREV
SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTQKQKKQHSVLHLVPIN
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREG
QGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIIPRARA KNLNLSPHGTFLGFVKL

Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

FIGURE 29

CACTTTCTCCCTCTCTTCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC
CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTA
CCGCCCCCACCCTCTCTTCTGCACTGCGCTCCTCGGAAGACCTTTTCCCTGCTCTGTT
TCCCTTCCAGAGTCTGTGCATCGCCCCGACCTGGCCGGGAGGAGCTTGGCCGGCGGGAGA
TGCTCTAGGGGGCGGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCGGACGGAAGATGGGC
TCCCGTGGACAGGACCTTGTGTGGCGTACTGCTGCTCTTGCCTTTGCTCTTGGCTGCTGTT
CCTGAGTCTGTGTGCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
CGTCGCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCACGTACG
GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCCTGCTGTGACCCCGGTACCTCCATGTACCC
GGCGACCGCGTGGCCAGATCAACATCACTATCTTGAAGGGGAGAGGGTGACCGCGGAG
ATCGAGGCTCCAAAGGAAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACACTGGA
CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTTGGGAGCGGTGCAAGAGCCACTACGCCCG
CTTTTCGGTGGGCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG
ACACGGATTCTGTGAACCTTACGACCATTCAACATGTTTACCGGCAAGTTCTACTGTCTAC
GTGCCCGGCTCTACTTCTTCACTCAACGTGCACACCTGGAACAGAGAGACCTACCT
GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTCGCGCAGGTGGGCGACCGCAGCA
TCATGCAAGCGCAGAGCTGTATGCTGGAGCTGCGAGAGCAGGACAGGTGTGGGTACGCCCT
TACAAGGGCGAACGTGAGAACGCCATCTTTCAGCGAGGAGCTGGACACCTACATCACCTTTCAG
TGCTTACTGTGTAAGCAGCCACCGAGCCCTAGCTGGCCGGCCACCTCTTCTCTCGCC
ACCTTCCACCCCTGCGCTGTGTGACCCCAACCGCTCTTCCCGCATCCCTGGAATCCGACT
CTGGCTTGTGCACTTACGTGAGACGCCCTGCAACAGAAAGCAAGCGATCGGTGCTTCC
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGACCCGCG
GAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCCTCAAGTGACCCCGCAGCGG
GAGACCGGGCTGGCGGAGGCGTCCAGGGTGGCGGACCGCGCTCCAGCTCTGGGATAAATA
ATTAGGCAAAATCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGAGGACAAAGAAAAGGG
TTGTATTTTGTCTTTCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCCCTTTTCAGTTGAG
ACTCTGCTTAAGAGACATCAAAGTTAAAGCTCTGGGGTCAAGGGAGGGCCGGGGCAGG
AAACTACCTCTGGCTTAATTTCTTTAAGCCACGTAGGAACCTTTCTGAGGGATAGGTGGACC
CTGACATCCCTGTGGCTTGGCCAAAGGGCTCTGCTGGTCTTTCTGAGTACAGCTCGGAGGT
GATGGGGGCTGGGCCCCAGGCGTCAGCTCCAGAGGGACAGCTGAGCCCTGCTTGGC
TCCAGGTTGGTAGAAGCCAGCGAAGGGCTCCTGACAGTGGCCAGGGACCCCTGGGTCCCCCA
GGCCTGCAGATGTTTCTATGAGGGGCGAGGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
ACCCCTGTGCCACCCCGAGAGCCCTGGGGGGTGGTCTCCATGCCTGCCACCTGGCATCGGCT
TTCTGTGCGGCTCCGACACAAATCAGCCCCAGAGGCGCCGGGCTTGGCTTCTGTTT
TATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCTCTGTGGCTAAGCATCACCGCTT
CCAGTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGAGCCCTTCTGCCCCCACTGCCCT
CATCAGGCTCTGACCAGTAGCTGAGAGGGGCTTTTCTAGGCTTCAGAGCAGGGGAGAG
CTGGAAGGGGCTAGAAAGCTCCGCTTGTCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCTGT
AGACCAGAGTCAAGAGGAATACAGCTCCCAATCACCGGTGTGAGGATCACTCTCAGGAGC
GTGTCTCCACGGTGTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCC
ATAGCCCTCTCCACCTCACCCATGTTGATGCCAGGGCTCACTGTGTACCCGTGGGG
CCCAAAACCCCGCTGCTCTCTTCTTCCCCCATCCCCACTGGTTTTCATTAATCTGCTG
TTCCCTCTCTGGGCGCTGCTCGCGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT
CTGCGGGTCAAGCTCTGAAGCCGAGTTGCTGTGGGCGTCCCGGAAGCAGAGCGCCCACTG
GCTGCTTAAGCTCCCCAGCTCTTTCAGAAAACATTAACTCAGAATTGTGTTTTCAA

09413760.024160

[illegible]

SECRET

SECRET

0607

[illegible]

0607

SECRET

0607

SECRET

[illegible]

SECRET

SECRET

SECRET

[illegible][illegible]

FIGURE 31

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGCGGATTGCGCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCGAGCTTCTTAAAGCAAATAGACCAGAGGGGAGATTAT
 CCTTGACCTTTTGAAGACCAAACCTAAACTGAAATTTAAATATGTTCTCTTCCGGGGGAGAGGGAG
 CTTGACTTACACTTTGGTAATAATTTGCTTCTTGACACTAAGGCTGTCTGTAGTCAGAAAT
 GCCTCAAAAAGAGCTAGAAAGATGTTGTCTTGACATCCAGTCATCTCTTCTAAGGGAATC
 AGAGGCAATGAGCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTCTGTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACTTGTATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAAATTTTCAAGCAGTCACCTCCC
 TAGCCCATCATCACACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCCTGAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAGCCCGCCACCCCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCCTCCCACGACCCCTCATTTCTACAGTTTTCACAGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACCGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCAAATTAACCTTGAACACAGGGAATGTTGATAACCCTA
 CTGCATTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAATGCTTCTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTCTCTGGTGTATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAAGGCCAAATGCAATGAGTTTCTGCTGACTTTGCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAAAATGCCCTTCTGCTTTCCTTTTCTTTTGGAGACAGATCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC
 CTGGGTTCAAGCGATTCTCCTGCCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTGTATTTTGTAGAGACGGGGTTTCACTAGTGTGGTCAGGCTG
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 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAGAAGGAATGAAGTG
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 ATGTAAAGTAATAAAGTATAAATTGCCATATAAAATTCAAAATTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCAATTCACATTTCTGGTTCCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGGATTCTTTAAAACTTATT
 CCAGATGTAGTTCCCTTCCAATTAATAATTGAATAAATCTTTTGTGTACTCAA

FIGURE 32

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLTVIICFLTLRLSASQNCCLKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMNSVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEEKWLLIGSLLFGVFLVLVIGLVLLGRILSESLRRKYSRLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

0967-866X

GCGGCACCTGGAAGATGTGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTCTGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGTCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCTGTCTCAAAGCTCCAGTCC
CCAAAAGGCAAAAATGTGACCACTGGACTCCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGAGGTGGCAGAAGCAAGTACGCCAAAACTGTCTTTGAGGATAACCTACTTATGGG
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ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTACAGAGTGTCTGCCAAAATCCCTGCTCTTCATGGTGACCTTAGCAGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTACAGGTCTAGCTGGGTATTTATTGCAGCAAAAAGGCTTGGAACCTCCCTTCCGAAATT
CAGAGAGAAAAGATCAACCACCTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTTGACATCGAGGCTCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTCTAAATCCAACA
GCCCATTTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGTAGTTGTATCA
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AACTAAATGAATGGAAATTTCTAAAAA

FIGURE 34

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777
><subunit 1 of 1, 235 aa, 1 stop
><MW: 25982, pI: 9.09, NX(S/T): 2
MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVVKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVITYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS
```

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125